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SEQUENCE LISTING

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Waterfield, Michael
Yonezawa, Kazu
Ludwig Institute for Cancer Research

<120> Identification and Functional Characterization of a
Novel Ribosomal S6 Protein Kinase

<130> 40750-5002-US

<140>

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<150> PCT/US99/17595
<151> 1999-08-04

<150> 60/095,268
<151> 1998-08-04

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<170> PatentIn Ver. 2.0

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<223> p70(beta) S6 Kinase gene

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gag ggc ttc tcc ttc cag ccc aag ctg cgc tca ccc agg cgc ctc aac 1360
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 Pro Pro Leu Leu Pro Pro Pro Pro Ser Thr Thr Ala Pro Leu Pro
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cca ggg cgc taggaagccg ggtgggggtg aggtagccc ttgagccctg 1601
 Pro Gly Arg
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Glu Thr Ser Val Asn Val Gly Pro Glu Arg Ile Gly Pro His Cys Phe
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Glu Leu Leu Arg Val Leu Gly Lys Gly Tyr Gly Lys Val Phe Gln
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Val Arg Lys Val Gln Gly Thr Asn Leu Gly Lys Ile Tyr Ala Met Lys
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Gly Ile Phe Leu Glu Asp Thr Ala Cys Phe Tyr Leu Ala Glu Ile Thr
180 185 190

Leu Ala Leu Gly His Leu His Ser Gln Gly Ile Ile Tyr Arg Asp Leu
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Lys Pro Glu Asn Ile Met Leu Ser Ser Gln Gly His Ile Lys Leu Thr
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 Asp Phe Gly Leu Cys Lys Glu Ser Ile His Glu Gly Ala Val Thr His
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 Thr Phe Cys Gly Thr Ile Glu Tyr Met Ala Pro Glu Ile Leu Val Arg
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 Ser Gly His Asn Arg Ala Val Asp Trp Trp Ser Leu Gly Ala Leu Met
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 Tyr Asp Met Leu Thr Gly Ser Pro Pro Phe Thr Ala Glu Asn Arg Lys
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 Lys Thr Met Asp Lys Ile Ile Arg Gly Lys Leu Ala Leu Pro Pro Tyr
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 Pro Ser Gln Arg Ile Gly Gly Pro Gly Asp Ala Ala Asp Val Gln
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 Ser Gln Phe Asp Thr Arg Phe Thr Arg Gln Thr Pro Val Asp Ser Pro
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 Thr Tyr Val Ala Pro Ser Val Leu Asp Ser Ile Lys Glu Gly Phe Ser
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 Phe Gln Pro Lys Leu Arg Ser Pro Arg Arg Leu Asn Ser Ser Pro Arg
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 Val Pro Val Ser Pro Leu Lys Phe Ser Pro Phe Glu Gly Phe Arg Pro
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 Ser Pro Ser Leu Pro Glu Pro Thr Glu Leu Pro Leu Pro Pro Leu Leu
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 Gly Val Phe Asp Ile Asp Leu Asp Gln Pro Glu Asp Ala Gly Ser Glu
 30 35 40

 gat gag ctg gag gag ggg ggt cag tta aat gaa agc atg gac cat ggg 198
 Asp Glu Leu Glu Gly Gln Leu Asn Glu Ser Met Asp His Gly
 45 50 55

 gga gtt gga cca tat gaa ctt ggc atg gaa cat tgt gag aaa ttt gaa 246
 Gly Val Gly Pro Tyr Glu Leu Gly Met Glu His Cys Glu Lys Phe Glu
 60 65 70

 atc tca gaa act agt gtg aac aga ggg cca gaa aaa atc aga cca gaa 294
 Ile Ser Glu Thr Ser Val Asn Arg Gly Pro Glu Lys Ile Arg Pro Glu
 75 80 85

 tgt ttt gag cta ctt cgg gta ctt ggt aaa ggg ggc tat gga aag gtt 342
 Cys Phe Glu Leu Leu Arg Val Leu Gly Lys Gly Tyr Gly Lys Val
 90 95 100 105

 ttt caa gta cga aaa gta aca gga gca aat act ggg aaa ata ttt gcc 390
 Phe Gln Val Arg Lys Val Thr Gly Ala Asn Thr Gly Lys Ile Phe Ala
 110 115 120

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 Met Lys Val Leu Lys Lys Ala Met Ile Val Arg Asn Ala Lys Asp Thr
 125 130 135

 gct cat aca aaa gca gaa cgg aat att ctg gag gaa gta aag cat ccc 486
 Ala His Thr Lys Ala Glu Arg Asn Ile Leu Glu Val Lys His Pro
 140 145 150

 ttc atc gtg gat tta att tat gcc ttt cag act ggt gga aaa ctc tac 534
 Phe Ile Val Asp Leu Ile Tyr Ala Phe Gln Thr Gly Gly Lys Leu Tyr
 155 160 165

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 Leu Ile Leu Glu Tyr Leu Ser Gly Gly Glu Leu Phe Met Gln Leu Glu

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Ile Ser Met Ala Leu Gly His Leu His Gln Lys Gly Ile Ile Tyr Arg				
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Asp Leu Lys Pro Glu Asn Ile Met Leu Asn His Gln Gly His Val Lys				
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cta aca gac ttt gga cta tgc aaa gaa tct att cat gat gga aca gtc				774
Leu Thr Asp Phe Gly Leu Cys Lys Glu Ser Ile His Asp Gly Thr Val				
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aca cac aca ttt tgt gga aca ata gaa tac atg gcc cct gaa atc ttg				822
Thr His Thr Phe Cys Gly Thr Ile Glu Tyr Met Ala Pro Glu Ile Leu				
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Leu Met Tyr Asp Met Leu Thr Gly Ala Pro Pro Phe Thr Gly Glu Asn				
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Arg Lys Lys Thr Ile Asp Lys Ile Leu Lys Cys Lys Leu Asn Leu Pro				
300	305	310		
ccc tac ctc aca caa gaa gcc aga gat ctg ctt aaa aag ctg ctg aaa				1014
Pro Tyr Leu Thr Gln Glu Ala Arg Asp Leu Leu Lys Lys Leu Leu Lys				
315	320	325		
aga aat gct tct cgt ctg gga gct ggt cct ggg gac gct gga gaa				1062
Arg Asn Ala Ala Ser Arg Leu Gly Ala Gly Pro Gly Asp Ala Gly Glu				
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gtt caa gct cat cca ttc ttt aga cac att aac tgg gaa gaa ctt ctg				1110
Val Gln Ala His Pro Phe Arg His Ile Asn Trp Glu Glu Leu Leu				
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gct cga aag gtg gag ccc ccc ttt aaa cct ctg ttg caa tct gaa gag				1158
Ala Arg Lys Val Glu Pro Pro Phe Lys Pro Leu Leu Gln Ser Glu Glu				
365	370	375		
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Asp Val Ser Gln Phe Asp Ser Lys Phe Thr Arg Gln Thr Pro Val Asp				
380	385	390		
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Ser Pro Asp Asp Ser Thr Leu Ser Glu Ser Ala Asn Gln Val Phe Leu				

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395

400

405

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cca cga aca cct gtc agc cca gtc aaa ttt tct cct ggg gat ttc tgg	445	450	455		1398
Pro Arg Thr Pro Val Ser Pro Val Lys Phe Ser Pro Gly Asp Phe Trp					
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Tyr Pro Met Glu Thr Ser Gly Ile Glu Gln Met Asp Val Thr Met Ser					
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Gly Glu Ala Ser Ala Pro Leu Pro Ile Arg Gln Pro Asn Ser Gly Pro					
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Arg Met Asn Leu					
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2346

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<213> Homo sapiens

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35 40 45

Gln Leu Asn Glu Ser Met Asp His Gly Gly Val Gly Pro Tyr Glu Leu
50 55 60

Gly Met Glu His Cys Glu Lys Phe Glu Ile Ser Glu Thr Ser Val Asn
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Arg Gly Pro Glu Lys Ile Arg Pro Glu Cys Phe Glu Leu Leu Arg Val
85 90 95

Leu Gly Lys Gly Tyr Gly Lys Val Phe Gln Val Arg Lys Val Thr
100 105 110

Gly Ala Asn Thr Gly Lys Ile Phe Ala Met Lys Val Leu Lys Lys Ala
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Ala Phe Gln Thr Gly Gly Lys Leu Tyr Leu Ile Leu Glu Tyr Leu Ser
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Gly Gly Glu Leu Phe Met Gln Leu Glu Arg Glu Gly Ile Phe Met Glu
180 185 190

Asp Thr Ala Cys Phe Tyr Leu Ala Glu Ile Ser Met Ala Leu Gly His
195 200 205

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210 215 220

Met Leu Asn His Gln Gly His Val Lys Leu Thr Asp Phe Gly Leu Cys
225 230 235 240

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260 265 270
Ala Val Asp Trp Trp Ser Leu Gly Ala Leu Met Tyr Asp Met Leu Thr
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Gly Ala Pro Pro Phe Thr Gly Glu Asn Arg Lys Lys Thr Ile Asp Lys
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Ile Leu Lys Cys Lys Leu Asn Leu Pro Pro Tyr Leu Thr Gln Glu Ala
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Gly Ala Gly Pro Gly Asp Ala Gly Glu Val Gln Ala His Pro Phe Phe
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Ser Gln Lys

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Gln Lys

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